

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: September 26, 2005, 18:32:48 ; Search time 1275.67 Seconds
(without alignments)
386.247 Million cell updates/sec

Title: US-09-581-528E-20

Perfect score: 1 tctgtcggagatgattgcacacacgaaagccc 36

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 25053377 seqs, 6843368929 residues

Total number of hits satisfying chosen parameters: 50106754

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Pending Patents NA.New.*
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
12: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
13: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
14: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
15: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
16: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
17: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
18: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
19: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
20: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
21: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
22: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
23: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
24: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
25: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
26: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33.2	92.2	36	US-09-581-528E-7	Sequence 7, Appl1
2	33.2	92.2	36	US-09-581-528E-8	Sequence 8, Appl1
3	33.2	92.2	36	US-09-581-528E-18	Sequence 18, Appl1
4	33.2	92.2	36	US-09-581-528E-19	Sequence 19, Appl1
5	33.2	92.2	36	US-09-581-528E-20	Sequence 20, Appl1
6	32.4	90.0	1404	US-09-581-528E-4	Sequence 4, Appl1
7	32.4	90.0	1929	US-11-070-405-3	Sequence 3, Appl1

8	32.4	90.0	1964	US-11-070-405-135	Sequence 135, App
9	31.6	87.8	1407	PCT-US04-42360-2316	Sequence 2316, App
10	31.6	87.8	1407	US-11-136-527-2454	Sequence 2454, App
11	26	72.2	201	US-60-659-397-5930	Sequence 5930, App
12	26	72.2	201	US-60-659-397-6011	Sequence 6011, App
13	26	72.2	201	US-60-659-397-6090	Sequence 6090, App
14	26	72.2	201	US-60-659-397-27095	Sequence 27095, A
15	25.2	70.0	201	US-60-659-397-5931	Sequence 5931, A
16	25.2	70.0	201	US-60-659-397-5933	Sequence 5933, App
17	25.2	70.0	201	US-60-659-397-5934	Sequence 5934, App
18	25.2	70.0	201	US-60-659-397-5935	Sequence 5935, App
19	25.2	70.0	201	US-60-659-397-5943	Sequence 5943, App
20	25.2	70.0	201	US-60-659-397-5944	Sequence 5944, App
21	25.2	70.0	201	US-60-659-397-6012	Sequence 6012, App
22	25.2	70.0	201	US-60-659-397-6013	Sequence 6013, App
23	25.2	70.0	201	US-60-659-397-6014	Sequence 6014, App
24	25.2	70.0	201	US-60-659-397-6015	Sequence 6015, App
25	25.2	70.0	201	US-60-659-397-6022	Sequence 6022, App
26	25.2	70.0	201	US-60-659-397-6089	Sequence 6089, App
27	25.2	70.0	201	US-60-659-397-6091	Sequence 6091, App
28	25.2	70.0	201	US-60-659-397-6092	Sequence 6092, App
29	25.2	70.0	201	US-60-659-397-6093	Sequence 6093, App
30	25.2	70.0	201	US-60-659-397-6094	Sequence 6094, App
31	25.2	70.0	201	US-60-659-397-6101	Sequence 6101, App
32	25.2	70.0	201	US-60-659-397-6101	Sequence 27098, A
33	25.2	70.0	201	US-60-659-397-27101	Sequence 27101, A
34	25.2	70.0	201	US-60-659-397-27105	Sequence 27105, A
35	25.2	70.0	201	US-60-659-397-27108	Sequence 27108, A
36	25.2	70.0	201	US-60-659-397-27124	Sequence 27124, A
37	25.2	70.0	201	US-60-659-397-27128	Sequence 27128, A
38	25.2	70.0	201	US-60-659-397-27201	Sequence 27201, A
39	25.2	70.0	469	US-11-070-405-63	Sequence 63, Appl1
40	25.2	70.0	489	US-11-070-405-74	Sequence 74, Appl1
41	25.2	70.0	498	US-11-070-405-62	Sequence 62, Appl1
42	25.2	70.0	500	US-11-070-405-108	Sequence 108, Appl1
43	25.2	70.0	945	US-11-070-405-6	Sequence 6, Appl1
44	25.2	70.0	945	US-11-070-405-160	Sequence 160, App
45	25.2	70.0	1404	US-09-581-528E-2	Sequence 2, Appl1

ALIGNMENTS

US-09-581-528E-7
Sequence 7, Application US/09581528E
GENERAL INFORMATION:
APPLICANT: TAKEDA, Masatoshi
TITLE OF INVENTION: Gene Mutant Animals
FILE REFERENCE: P19743
CURRENT APPLICATION NUMBER: US/09/581,528E
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: PCT/JP99/00015
PRIOR FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: Primer
US-09-581-528E-7

Query Match 92.2% Score 33.2; DB 6; Length 36;
Best Local Similarity 88.9%; Pred. No. 0.0013; 0;
Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
DB 1 TGTGTCGGAGATGATGCGCCVVCACCTGGAAGGCC 36
1 TGTGTCGGAGATGATGCGCCACCACTGGAAGGCC 36

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:29:14 ; Search time 2455 Seconds
(without alignments)
598.627 Million cell updates/sec

Title: US-09-581-528E-20

Sequence: 1 tctgttcgagatgacgacccgaaagccc 36

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_NA_Main.*
1: /cgn2_6/ptodata/1/pna/US0999F_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US0999G_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US0999H_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US0999I_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US0999J_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US0999K_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US0999L_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US0999M_COMB.seq.*
9: /cgn2_6/ptodata/1/pna/US0999N_COMB.seq.*
10: /cgn2_6/ptodata/1/pna/US0999O_COMB.seq.*
11: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
12: /cgn2_6/ptodata/1/pna/US0999Q_COMB.seq.*
13: /cgn2_6/ptodata/1/pna/US0999R_COMB.seq.*
14: /cgn2_6/ptodata/1/pna/US0999S_COMB.seq.*
15: /cgn2_6/ptodata/1/pna/US0999T_COMB.seq.*
16: /cgn2_6/ptodata/1/pna/US0999U_COMB.seq.*
17: /cgn2_6/ptodata/1/pna/US0999V_COMB.seq.*
18: /cgn2_6/ptodata/1/pna/US0999W_COMB.seq.*
19: /cgn2_6/ptodata/1/pna/US0999X_COMB.seq.*
20: /cgn2_6/ptodata/1/pna/US0999Y_COMB.seq.*
21: /cgn2_6/ptodata/1/pna/US0999Z_COMB.seq.*
22: /cgn2_6/ptodata/1/pna/US0999A_COMB.seq.*
23: /cgn2_6/ptodata/1/pna/US0999B_COMB.seq.*
24: /cgn2_6/ptodata/1/pna/US0999C_COMB.seq.*
25: /cgn2_6/ptodata/1/pna/US0999D_COMB.seq.*
26: /cgn2_6/ptodata/1/pna/US0999E_COMB.seq.*
27: /cgn2_6/ptodata/1/pna/US0999F_COMB.seq.*
28: /cgn2_6/ptodata/1/pna/US0999G_COMB.seq.*
29: /cgn2_6/ptodata/1/pna/US0999H_COMB.seq.*
30: /cgn2_6/ptodata/1/pna/US0999I_COMB.seq.*
31: /cgn2_6/ptodata/1/pna/US0999J_COMB.seq.*
32: /cgn2_6/ptodata/1/pna/US0999K_COMB.seq.*
33: /cgn2_6/ptodata/1/pna/US0999L_COMB.seq.*
34: /cgn2_6/ptodata/1/pna/US0999M_COMB.seq.*
35: /cgn2_6/ptodata/1/pna/US0999N_COMB.seq.*
36: /cgn2_6/ptodata/1/pna/US0999O_COMB.seq.*
37: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
38: /cgn2_6/ptodata/1/pna/US0999Q_COMB.seq.*
39: /cgn2_6/ptodata/1/pna/US0999R_COMB.seq.*
40: /cgn2_6/ptodata/1/pna/US0999S_COMB.seq.*
41: /cgn2_6/ptodata/1/pna/US0999T_COMB.seq.*
42: /cgn2_6/ptodata/1/pna/US0999U_COMB.seq.*
43: /cgn2_6/ptodata/1/pna/US0999V_COMB.seq.*

44: /cgn2_6/ptodata/1/pna/US0999F_COMB.seq.*
45: /cgn2_6/ptodata/1/pna/US0999G_COMB.seq.*
46: /cgn2_6/ptodata/1/pna/US0999H_COMB.seq.*
47: /cgn2_6/ptodata/1/pna/US0999I_COMB.seq.*
48: /cgn2_6/ptodata/1/pna/US0999J_COMB.seq.*
49: /cgn2_6/ptodata/1/pna/US0999K_COMB.seq.*
50: /cgn2_6/ptodata/1/pna/US0999L_COMB.seq.*
51: /cgn2_6/ptodata/1/pna/US0999M_COMB.seq.*
52: /cgn2_6/ptodata/1/pna/US0999N_COMB.seq.*
53: /cgn2_6/ptodata/1/pna/US0999O_COMB.seq.*
54: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
55: /cgn2_6/ptodata/1/pna/US0999Q_COMB.seq.*
56: /cgn2_6/ptodata/1/pna/US0999R_COMB.seq.*
57: /cgn2_6/ptodata/1/pna/US0999S_COMB.seq.*
58: /cgn2_6/ptodata/1/pna/US0999T_COMB.seq.*
59: /cgn2_6/ptodata/1/pna/US0999U_COMB.seq.*
60: /cgn2_6/ptodata/1/pna/US0999V_COMB.seq.*
61: /cgn2_6/ptodata/1/pna/US0999W_COMB.seq.*
62: /cgn2_6/ptodata/1/pna/US0999X_COMB.seq.*
63: /cgn2_6/ptodata/1/pna/US0999Y_COMB.seq.*
64: /cgn2_6/ptodata/1/pna/US0999Z_COMB.seq.*
65: /cgn2_6/ptodata/1/pna/US0999A_COMB.seq.*
66: /cgn2_6/ptodata/1/pna/US0999B_COMB.seq.*
67: /cgn2_6/ptodata/1/pna/US0999C_COMB.seq.*
68: /cgn2_6/ptodata/1/pna/US0999D_COMB.seq.*
69: /cgn2_6/ptodata/1/pna/US0999E_COMB.seq.*
70: /cgn2_6/ptodata/1/pna/US0999F_COMB.seq.*
71: /cgn2_6/ptodata/1/pna/US0999G_COMB.seq.*
72: /cgn2_6/ptodata/1/pna/US0999H_COMB.seq.*
73: /cgn2_6/ptodata/1/pna/US0999I_COMB.seq.*
74: /cgn2_6/ptodata/1/pna/US0999J_COMB.seq.*
75: /cgn2_6/ptodata/1/pna/US0999K_COMB.seq.*
76: /cgn2_6/ptodata/1/pna/US0999L_COMB.seq.*
77: /cgn2_6/ptodata/1/pna/US0999M_COMB.seq.*
78: /cgn2_6/ptodata/1/pna/US0999N_COMB.seq.*
79: /cgn2_6/ptodata/1/pna/US0999O_COMB.seq.*
80: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
81: /cgn2_6/ptodata/1/pna/US0999Q_COMB.seq.*
82: /cgn2_6/ptodata/1/pna/US0999R_COMB.seq.*
83: /cgn2_6/ptodata/1/pna/US0999S_COMB.seq.*
84: /cgn2_6/ptodata/1/pna/US0999T_COMB.seq.*
85: /cgn2_6/ptodata/1/pna/US0999U_COMB.seq.*
86: /cgn2_6/ptodata/1/pna/US0999V_COMB.seq.*
87: /cgn2_6/ptodata/1/pna/US0999W_COMB.seq.*
88: /cgn2_6/ptodata/1/pna/US0999X_COMB.seq.*
89: /cgn2_6/ptodata/1/pna/US0999Y_COMB.seq.*
90: /cgn2_6/ptodata/1/pna/US0999Z_COMB.seq.*
91: /cgn2_6/ptodata/1/pna/US0999A_COMB.seq.*
92: /cgn2_6/ptodata/1/pna/US0999B_COMB.seq.*
93: /cgn2_6/ptodata/1/pna/US0999C_COMB.seq.*
94: /cgn2_6/ptodata/1/pna/US0999D_COMB.seq.*
95: /cgn2_6/ptodata/1/pna/US0999E_COMB.seq.*
96: /cgn2_6/ptodata/1/pna/US0999F_COMB.seq.*
97: /cgn2_6/ptodata/1/pna/US0999G_COMB.seq.*
98: /cgn2_6/ptodata/1/pna/US0999H_COMB.seq.*
99: /cgn2_6/ptodata/1/pna/US0999I_COMB.seq.*
100: /cgn2_6/ptodata/1/pna/US0999J_COMB.seq.*
101: /cgn2_6/ptodata/1/pna/US0999K_COMB.seq.*
102: /cgn2_6/ptodata/1/pna/US0999L_COMB.seq.*
103: /cgn2_6/ptodata/1/pna/US0999M_COMB.seq.*
104: /cgn2_6/ptodata/1/pna/US0999N_COMB.seq.*
105: /cgn2_6/ptodata/1/pna/US0999O_COMB.seq.*
106: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
107: /cgn2_6/ptodata/1/pna/US0999Q_COMB.seq.*
108: /cgn2_6/ptodata/1/pna/US0999R_COMB.seq.*
109: /cgn2_6/ptodata/1/pna/US0999S_COMB.seq.*
110: /cgn2_6/ptodata/1/pna/US0999T_COMB.seq.*
111: /cgn2_6/ptodata/1/pna/US0999U_COMB.seq.*
112: /cgn2_6/ptodata/1/pna/US0999V_COMB.seq.*
113: /cgn2_6/ptodata/1/pna/US0999W_COMB.seq.*
114: /cgn2_6/ptodata/1/pna/US0999X_COMB.seq.*
115: /cgn2_6/ptodata/1/pna/US0999Y_COMB.seq.*
116: /cgn2_6/ptodata/1/pna/US0999Z_COMB.seq.*

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:33:43 / Search time 362.333 Seconds
(without alignments)
664.322 Million cell updates/sec

Title: US-09-581-528E-20

Perfect score: 1 tctgtcgggatgatygccvvcacatcgaaagccc 36

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 7400732 seqs, 3343137571 residues

Total number of hits satisfying chosen parameters: 14801464

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications NA:*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/1/pubpna/PCr_NEM_PUB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEM_PUB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEM_PUB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/PCrUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEM_PUB.seq:*
- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/prodata/1/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/prodata/1/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/prodata/1/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/prodata/1/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32.4	90.0	221	21	US-10-957-311-8
2	32.4	90.0	221	21	US-10-957-311-9
3	25.2	70.0	121	10	US-09-818-875-4196
4	25.2	70.0	121	10	US-09-818-875-4197
5	25.2	70.0	121	10	US-09-818-875-4200
6	25.2	70.0	121	10	US-09-818-875-4201
7	25.2	70.0	121	10	US-09-818-875-4204

C	8	25.2	70.0	121	10	US-09-818-875-4205	Sequence 4205, Ap
C	9	25.2	70.0	121	10	US-09-818-875-4208	Sequence 4208, Ap
C	10	25.2	70.0	121	10	US-09-818-875-4209	Sequence 4209, Ap
C	11	25.2	70.0	121	17	US-10-209-787-4196	Sequence 4196, Ap
C	12	25.2	70.0	121	17	US-10-209-787-4197	Sequence 4197, Ap
C	13	25.2	70.0	121	17	US-10-209-787-4200	Sequence 4200, Ap
C	14	25.2	70.0	121	17	US-10-209-787-4201	Sequence 4201, Ap
C	15	25.2	70.0	121	17	US-10-209-787-4204	Sequence 4204, Ap
C	16	25.2	70.0	121	17	US-10-209-787-4205	Sequence 4205, Ap
C	17	25.2	70.0	121	17	US-10-209-787-4208	Sequence 4208, Ap
C	18	25.2	70.0	121	17	US-10-209-787-4209	Sequence 4209, Ap
C	19	25.2	70.0	121	17	US-10-261-185-4196	Sequence 4196, Ap
C	20	25.2	70.0	121	17	US-10-261-185-4197	Sequence 4197, Ap
C	21	25.2	70.0	121	17	US-10-261-185-4201	Sequence 4201, Ap
C	22	25.2	70.0	121	17	US-10-261-185-4204	Sequence 4204, Ap
C	23	25.2	70.0	121	17	US-10-261-185-4205	Sequence 4205, Ap
C	24	25.2	70.0	121	17	US-10-261-185-4208	Sequence 4208, Ap
C	25	25.2	70.0	121	17	US-10-261-185-4209	Sequence 4209, Ap
C	26	25.2	70.0	121	17	US-10-681-074-4196	Sequence 4196, Ap
C	27	25.2	70.0	121	19	US-10-681-074-4197	Sequence 4197, Ap
C	28	25.2	70.0	121	19	US-10-681-074-4201	Sequence 4201, Ap
C	29	25.2	70.0	121	19	US-10-681-074-4204	Sequence 4204, Ap
C	30	25.2	70.0	121	19	US-10-681-074-4205	Sequence 4205, Ap
C	31	25.2	70.0	121	19	US-10-681-074-4208	Sequence 4208, Ap
C	32	25.2	70.0	121	19	US-10-681-074-4209	Sequence 4209, Ap
C	33	25.2	70.0	121	19	US-10-681-074-4205	Sequence 4205, Ap
C	34	25.2	70.0	121	19	US-10-681-074-4208	Sequence 4208, Ap
C	35	25.2	70.0	121	16	US-10-029-386-16073	Sequence 16073, A
C	36	25.2	70.0	411	16	US-10-029-386-4373	Sequence 4373, A
C	37	25.2	70.0	1254	22	US-10-504-173-4	Sequence 4, Appl1
C	38	25.2	70.0	1382	9	US-09-895-035-13	Sequence 13, Appl1
C	39	25.2	70.0	1392	20	US-10-888-004-13	Sequence 3, Appl1
C	40	25.2	70.0	1404	9	US-09-754-949-3	Sequence 1, Appl1
C	41	25.2	70.0	1404	10	US-09-896-621B-1	Sequence 2, Appl1
C	42	25.2	70.0	1404	10	US-09-896-621B-2	Sequence 3, Appl1
C	43	25.2	70.0	1404	10	US-09-896-621B-3	Sequence 4, Appl1
C	44	25.2	70.0	1404	17	US-10-417-422-3	Sequence 7, Appl1
C	45	25.2	70.0	2763	16	US-10-293-000-7	

ALIGNMENTS

RESULT 1
US-10-957-311-8
Sequence 8, Appl1
Publication No. US20050076400A1
GENERAL INFORMATION:
APPLICANT: CASAS LOUZA, Caty
APPLICANT: BENOIT, Patrick
APPLICANT: PRADIER, Laurent
APPLICANT: TREMP, Gunter
APPLICANT: IITER, Jean-Michel
TITLE OF INVENTION: TRANSGENIC ANIMALS EXHIBITTING MAJOR DISORDERS RELATED TO
FILE REFERENCE: FRAV2003/0027 US NP
CURRENT APPLICATION NUMBER: US/10/957,311
PRIOR FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: US 60/523,397
PRIOR FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: FR 0311578
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 221
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Murine PSI Exon 7 Containing Mutations
US-10-957-311-8

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:28:37 ; Search time 69.6667 seconds
(without alignments)
845.540 Million cell updates/sec

Title: US-09-581-528E-20

Perfect score: 36
Sequence: 1 tgcgtcgagatgatygcvtvccatcgaaagcc 36

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32.4	90.0	1636	4	US-09-544-618-16 Sequence 16, Appl
2	32.4	90.0	1929	2	US-08-967-101-3 Sequence 3, Appl
3	32.4	90.0	1929	2	US-08-592-541-3 Sequence 3, Appl
4	32.4	90.0	1929	3	US-09-124-698-3 Sequence 3, Appl
5	32.4	90.0	1929	3	US-09-127-480-3 Sequence 3, Appl
6	32.4	90.0	1929	3	US-08-496-841C-3 Sequence 3, Appl
7	32.4	90.0	1929	3	US-09-124-523-3 Sequence 3, Appl
8	32.4	90.0	1929	4	US-09-636-796A-3 Sequence 3, Appl
9	32.4	90.0	1929	4	US-08-431-048F-3 Sequence 3, Appl
10	32.4	90.0	1962	2	US-08-967-101-135 Sequence 135, App
11	32.4	90.0	1962	2	US-08-592-541-135 Sequence 135, App
12	32.4	90.0	1962	3	US-09-124-698-135 Sequence 135, App
13	32.4	90.0	1962	3	US-09-127-480-135 Sequence 135, App
14	32.4	90.0	1962	4	US-09-124-523-135 Sequence 135, App
15	32.4	90.0	1962	4	US-09-636-796A-135 Sequence 135, App
16	32.4	90.0	1964	3	US-08-888-077A-16 Sequence 16, Appl
17	32.4	90.0	1964	3	US-08-496-841C-135 Sequence 135, App
18	32.4	90.0	2680	4	US-09-382-396-2 Sequence 2, Appl
19	32.4	90.0	2681	4	US-09-544-618-10 Sequence 10, Appl
20	32.4	90.0	48974	3	US-08-920-422-17 Sequence 17, Appl
21	25.2	70.0	469	2	US-08-967-101-63 Sequence 63, Appl
22	25.2	70.0	469	2	US-08-592-541-63 Sequence 63, Appl
23	25.2	70.0	469	3	US-09-124-698-63 Sequence 63, Appl
24	25.2	70.0	469	3	US-09-127-480-63 Sequence 63, Appl
25	25.2	70.0	469	3	US-08-496-841C-63 Sequence 63, Appl
26	25.2	70.0	469	3	US-09-124-523-63 Sequence 63, Appl
27	25.2	70.0	469	4	US-09-636-796A-63 Sequence 63, Appl

C	28	25.2	70.0	469	4	US-08-431-048F-63 Sequence 63, Appl
	29	25.2	70.0	469	2	US-08-967-101-74 Sequence 74, Appl
	30	25.2	70.0	469	2	US-08-592-541-74 Sequence 74, Appl
	31	25.2	70.0	469	3	US-09-124-698-74 Sequence 74, Appl
	32	25.2	70.0	469	3	US-09-127-480-74 Sequence 74, Appl
	33	25.2	70.0	469	3	US-08-496-841C-74 Sequence 74, Appl
	34	25.2	70.0	469	3	US-09-124-523-74 Sequence 74, Appl
	35	25.2	70.0	469	4	US-09-636-796A-74 Sequence 74, Appl
	36	25.2	70.0	469	4	US-08-431-048F-74 Sequence 74, Appl
C	37	25.2	70.0	469	2	US-08-967-101-62 Sequence 62, Appl
C	38	25.2	70.0	469	2	US-08-592-541-62 Sequence 62, Appl
C	39	25.2	70.0	469	3	US-09-124-698-62 Sequence 62, Appl
C	40	25.2	70.0	469	3	US-09-127-480-62 Sequence 62, Appl
C	41	25.2	70.0	469	3	US-08-496-841C-62 Sequence 62, Appl
C	42	25.2	70.0	469	3	US-09-124-523-62 Sequence 62, Appl
C	43	25.2	70.0	469	4	US-09-636-796A-62 Sequence 62, Appl
C	44	25.2	70.0	469	4	US-08-431-048F-62 Sequence 62, Appl
C	45	25.2	70.0	500	2	US-08-967-101-108 Sequence 108, App

ALIGNMENTS

RESULT 1
US-09-544-618-16
Sequence 16, Application US/09544618
Patent No. 6503502
GENERAL INFORMATION:
APPLICANT: Telerman, Adam
APPLICANT: Amson, Robert
APPLICANT: Cohen, Daniel
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
FILE REFERENCE: 065691-0139
CURRENT APPLICATION NUMBER: US/09/544,618
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 1636
TYPE: DNA
ORGANISM: MOUSE
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1636)
OTHER INFORMATION: applicants are unsure of various bases designated as "n"
US-09-544-618-16
Query Match 90.0%; Score 32.4; DB 4; Length 1636;
Best Local Similarity 88.9%; Pred. No. 0.00028;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGTGTCGGATGATTCGCTGAAAGGCC 36
DB 806 TGTGTCGGATGATTCGCTGAAAGGCC 841
RESULT 2
US-08-967-101-3
Sequence 3, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSER: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: September 26, 2005, 18:32:48 ; Search time 1275.67 Seconds
(without alignments)
386.247 Million cell updates/sec

Title: US-09-581-528E-19

Sequence: 1 tctgtcggatgattgacacacactggaagcc 36

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 25053377 seqs, 6843368929 residues

Total number of hits satisfying chosen parameters: 50106754

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents, NA New:*

1: /cgn2_6/ptodata/1/pna/PCT NEW COMB. seq:*

2: /cgn2_6/ptodata/1/pna/PCT NEW COMB. seq:*

3: /cgn2_6/ptodata/1/pna/US06 NEW COMB. seq:*

4: /cgn2_6/ptodata/1/pna/US07 NEW COMB. seq:*

5: /cgn2_6/ptodata/1/pna/US08 NEW COMB. seq:*

6: /cgn2_6/ptodata/1/pna/US09 NEW COMB. seq:*

7: /cgn2_6/ptodata/1/pna/US09 NEW COMB. seq:*

8: /cgn2_6/ptodata/1/pna/US09 NEW COMB. seq:*

9: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

10: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

11: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

12: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

13: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

14: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

15: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

16: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

17: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

18: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

19: /cgn2_6/ptodata/1/pna/US10 NEW COMB. seq:*

20: /cgn2_6/ptodata/1/pna/US11 NEW COMB. seq:*

21: /cgn2_6/ptodata/1/pna/US11 NEW COMB. seq:*

22: /cgn2_6/ptodata/1/pna/US11 NEW COMB. seq:*

23: /cgn2_6/ptodata/1/pna/US11 NEW COMB. seq:*

24: /cgn2_6/ptodata/1/pna/US11 NEW COMB. seq:*

25: /cgn2_6/ptodata/1/pna/US11 NEW COMB. seq:*

26: /cgn2_6/ptodata/1/pna/US60 NEW COMB. seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	34.8	96.7	36	US-09-581-528E-7
2	34.8	96.7	36	US-09-581-528E-8
3	34.8	96.7	36	US-09-581-528E-18
4	34.8	96.7	36	US-09-581-528E-19
5	34	94.4	6	US-09-581-528E-3
6	34	94.4	6	US-11-070-405-4
7	34	94.4	24	US-11-070-405-135

8	33.2	92.2	35	6	US-09-581-528E-20	Sequence 20, Appl
9	32.4	90.0	1407	2	PCT-US04-42360-2316	Sequence 2316, Ap
10	32.4	90.0	1407	24	US-11-136-527-2454	Sequence 2454, Ap
11	26.8	74.4	201	26	US-60-659-397-5930	Sequence 5930, Ap
12	26.8	74.4	201	26	US-60-659-397-6011	Sequence 6011, Ap
13	26.8	74.4	201	26	US-60-659-397-6090	Sequence 6090, Ap
14	26.8	74.4	201	26	US-60-659-397-27095	Sequence 27095, A
15	26	72.2	201	26	US-60-659-397-5931	Sequence 5931, Ap
16	26	72.2	201	26	US-60-659-397-5933	Sequence 5933, Ap
17	26	72.2	201	26	US-60-659-397-5934	Sequence 5934, Ap
18	26	72.2	201	26	US-60-659-397-5935	Sequence 5935, Ap
19	26	72.2	201	26	US-60-659-397-5943	Sequence 5943, Ap
20	26	72.2	201	26	US-60-659-397-6010	Sequence 6010, Ap
21	26	72.2	201	26	US-60-659-397-6012	Sequence 6012, Ap
22	26	72.2	201	26	US-60-659-397-6013	Sequence 6013, Ap
23	26	72.2	201	26	US-60-659-397-6014	Sequence 6014, Ap
24	26	72.2	201	26	US-60-659-397-6015	Sequence 6015, Ap
25	26	72.2	201	26	US-60-659-397-6022	Sequence 6022, Ap
26	26	72.2	201	26	US-60-659-397-6089	Sequence 6089, Ap
27	26	72.2	201	26	US-60-659-397-6091	Sequence 6091, Ap
28	26	72.2	201	26	US-60-659-397-6092	Sequence 6092, Ap
29	26	72.2	201	26	US-60-659-397-6093	Sequence 6093, Ap
30	26	72.2	201	26	US-60-659-397-6094	Sequence 6094, Ap
31	26	72.2	201	26	US-60-659-397-6101	Sequence 6101, Ap
32	26	72.2	201	26	US-60-659-397-27098	Sequence 27098, A
33	26	72.2	201	26	US-60-659-397-27101	Sequence 27101, A
34	26	72.2	201	26	US-60-659-397-27105	Sequence 27105, A
35	26	72.2	201	26	US-60-659-397-27108	Sequence 27108, A
36	26	72.2	201	26	US-60-659-397-27124	Sequence 27124, A
37	26	72.2	201	26	US-60-659-397-27201	Sequence 27201, A
38	26	72.2	201	26	US-60-659-397-405-63	Sequence 63, Appl
39	26	72.2	469	24	US-11-070-405-74	Sequence 74, Appl
40	26	72.2	489	24	US-11-070-405-62	Sequence 62, Appl
41	26	72.2	498	24	US-11-070-405-108	Sequence 108, Appl
42	26	72.2	500	24	US-11-070-405-160	Sequence 160, Appl
43	26	72.2	945	24	US-11-070-405-6	Sequence 6, Appl
44	26	72.2	945	24	US-11-070-405-160	Sequence 160, Appl
45	26	72.2	1404	6	US-09-581-528E-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-581-528E-7
; Sequence 7, Application US/09581528E
; GENERAL INFORMATION:
; APPLICANT: TAKEDA, Junji
; TITLE OF INVENTION: Gene Mutant Animals
; FILE REFERENCE: P19743
; CURRENT APPLICATION NUMBER: US/09/581,528E
; PRIOR APPLICATION NUMBER: 2000-10-26
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: Primer
US-09-581-528E-7

Query Match	Score 34.8;	DB 6;	Length 36;
Best Local Similarity	94.4%;	Pred. No. 0.00037;	
Matches 34;	Conservative 2;	Mismatches 0;	Indels 0;

Query 1 tctgtcggatgattgacacacactggaagcc 36
DB 1 tctgtcggatgattgacacacactggaagcc 36

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:29:14 ; Search time 2455 Seconds
(without alignments)
598.627 Million cell updates/sec

Title: US-09-581-528B-19
Sequence: 1 tctgtcggagatgacccavccactggaagcccc 36

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents_NA_Main:*

- 1: /cgn2_6/ptodata/1/pna/US0999_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US0998_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US0997_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US0996_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US0995_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US0994_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US0993_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US0992_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US0991_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US0990_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US0989_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US0988_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US0987_COMB.seq.*
- 14: /cgn2_6/ptodata/1/pna/US0986_COMB.seq.*
- 15: /cgn2_6/ptodata/1/pna/US0985_COMB.seq.*
- 16: /cgn2_6/ptodata/1/pna/US0984_COMB.seq.*
- 17: /cgn2_6/ptodata/1/pna/US0983_COMB.seq.*
- 18: /cgn2_6/ptodata/1/pna/US0982_COMB.seq.*
- 19: /cgn2_6/ptodata/1/pna/US0981_COMB.seq.*
- 20: /cgn2_6/ptodata/1/pna/US0980_COMB.seq.*
- 21: /cgn2_6/ptodata/1/pna/US0979_COMB.seq.*
- 22: /cgn2_6/ptodata/1/pna/US0978_COMB.seq.*
- 23: /cgn2_6/ptodata/1/pna/US0977_COMB.seq.*
- 24: /cgn2_6/ptodata/1/pna/US0976_COMB.seq.*
- 25: /cgn2_6/ptodata/1/pna/US0975_COMB.seq.*
- 26: /cgn2_6/ptodata/1/pna/US0974_COMB.seq.*
- 27: /cgn2_6/ptodata/1/pna/US0973_COMB.seq.*
- 28: /cgn2_6/ptodata/1/pna/US0972_COMB.seq.*
- 29: /cgn2_6/ptodata/1/pna/US0971_COMB.seq.*
- 30: /cgn2_6/ptodata/1/pna/US0970_COMB.seq.*
- 31: /cgn2_6/ptodata/1/pna/US0969_COMB.seq.*
- 32: /cgn2_6/ptodata/1/pna/US0968_COMB.seq.*
- 33: /cgn2_6/ptodata/1/pna/US0967_COMB.seq.*
- 34: /cgn2_6/ptodata/1/pna/US0966_COMB.seq.*
- 35: /cgn2_6/ptodata/1/pna/US0965_COMB.seq.*
- 36: /cgn2_6/ptodata/1/pna/US0964_COMB.seq.*
- 37: /cgn2_6/ptodata/1/pna/US0963_COMB.seq.*
- 38: /cgn2_6/ptodata/1/pna/US0962_COMB.seq.*
- 39: /cgn2_6/ptodata/1/pna/US0961_COMB.seq.*
- 40: /cgn2_6/ptodata/1/pna/US0960_COMB.seq.*
- 41: /cgn2_6/ptodata/1/pna/US0959_COMB.seq.*
- 42: /cgn2_6/ptodata/1/pna/US0958_COMB.seq.*
- 43: /cgn2_6/ptodata/1/pna/US0957_COMB.seq.*

- 44: /cgn2_6/ptodata/1/pna/US0999_COMB.seq.*
- 45: /cgn2_6/ptodata/1/pna/US0998_COMB.seq.*
- 46: /cgn2_6/ptodata/1/pna/US0997_COMB.seq.*
- 47: /cgn2_6/ptodata/1/pna/US0996_COMB.seq.*
- 48: /cgn2_6/ptodata/1/pna/US0995_COMB.seq.*
- 49: /cgn2_6/ptodata/1/pna/US0994_COMB.seq.*
- 50: /cgn2_6/ptodata/1/pna/US0993_COMB.seq.*
- 51: /cgn2_6/ptodata/1/pna/US0992_COMB.seq.*
- 52: /cgn2_6/ptodata/1/pna/US0991_COMB.seq.*
- 53: /cgn2_6/ptodata/1/pna/US0990_COMB.seq.*
- 54: /cgn2_6/ptodata/1/pna/US0989_COMB.seq.*
- 55: /cgn2_6/ptodata/1/pna/US0988_COMB.seq.*
- 56: /cgn2_6/ptodata/1/pna/US0987_COMB.seq.*
- 57: /cgn2_6/ptodata/1/pna/US0986_COMB.seq.*
- 58: /cgn2_6/ptodata/1/pna/US0985_COMB.seq.*
- 59: /cgn2_6/ptodata/1/pna/US0984_COMB.seq.*
- 60: /cgn2_6/ptodata/1/pna/US0983_COMB.seq.*
- 61: /cgn2_6/ptodata/1/pna/US0982_COMB.seq.*
- 62: /cgn2_6/ptodata/1/pna/US0981_COMB.seq.*
- 63: /cgn2_6/ptodata/1/pna/US0980_COMB.seq.*
- 64: /cgn2_6/ptodata/1/pna/US0979_COMB.seq.*
- 65: /cgn2_6/ptodata/1/pna/US0978_COMB.seq.*
- 66: /cgn2_6/ptodata/1/pna/US0977_COMB.seq.*
- 67: /cgn2_6/ptodata/1/pna/US0976_COMB.seq.*
- 68: /cgn2_6/ptodata/1/pna/US0975_COMB.seq.*
- 69: /cgn2_6/ptodata/1/pna/US0974_COMB.seq.*
- 70: /cgn2_6/ptodata/1/pna/US0973_COMB.seq.*
- 71: /cgn2_6/ptodata/1/pna/US0972_COMB.seq.*
- 72: /cgn2_6/ptodata/1/pna/US0971_COMB.seq.*
- 73: /cgn2_6/ptodata/1/pna/US0970_COMB.seq.*
- 74: /cgn2_6/ptodata/1/pna/US0969_COMB.seq.*
- 75: /cgn2_6/ptodata/1/pna/US0968_COMB.seq.*
- 76: /cgn2_6/ptodata/1/pna/US0967_COMB.seq.*
- 77: /cgn2_6/ptodata/1/pna/US0966_COMB.seq.*
- 78: /cgn2_6/ptodata/1/pna/US0965_COMB.seq.*
- 79: /cgn2_6/ptodata/1/pna/US0964_COMB.seq.*
- 80: /cgn2_6/ptodata/1/pna/US0963_COMB.seq.*
- 81: /cgn2_6/ptodata/1/pna/US0962_COMB.seq.*
- 82: /cgn2_6/ptodata/1/pna/US0961_COMB.seq.*
- 83: /cgn2_6/ptodata/1/pna/US0960_COMB.seq.*
- 84: /cgn2_6/ptodata/1/pna/US0959_COMB.seq.*
- 85: /cgn2_6/ptodata/1/pna/US0958_COMB.seq.*
- 86: /cgn2_6/ptodata/1/pna/US0957_COMB.seq.*
- 87: /cgn2_6/ptodata/1/pna/US0956_COMB.seq.*
- 88: /cgn2_6/ptodata/1/pna/US0955_COMB.seq.*
- 89: /cgn2_6/ptodata/1/pna/US0954_COMB.seq.*
- 90: /cgn2_6/ptodata/1/pna/US0953_COMB.seq.*
- 91: /cgn2_6/ptodata/1/pna/US0952_COMB.seq.*
- 92: /cgn2_6/ptodata/1/pna/US0951_COMB.seq.*
- 93: /cgn2_6/ptodata/1/pna/US0950_COMB.seq.*
- 94: /cgn2_6/ptodata/1/pna/US0949_COMB.seq.*
- 95: /cgn2_6/ptodata/1/pna/US0948_COMB.seq.*
- 96: /cgn2_6/ptodata/1/pna/US0947_COMB.seq.*
- 97: /cgn2_6/ptodata/1/pna/US0946_COMB.seq.*
- 98: /cgn2_6/ptodata/1/pna/US0945_COMB.seq.*
- 99: /cgn2_6/ptodata/1/pna/US0944_COMB.seq.*
- 100: /cgn2_6/ptodata/1/pna/US0943_COMB.seq.*
- 101: /cgn2_6/ptodata/1/pna/US0942_COMB.seq.*
- 102: /cgn2_6/ptodata/1/pna/US0941_COMB.seq.*
- 103: /cgn2_6/ptodata/1/pna/US0940_COMB.seq.*
- 104: /cgn2_6/ptodata/1/pna/US0939_COMB.seq.*
- 105: /cgn2_6/ptodata/1/pna/US0938_COMB.seq.*
- 106: /cgn2_6/ptodata/1/pna/US0937_COMB.seq.*
- 107: /cgn2_6/ptodata/1/pna/US0936_COMB.seq.*
- 108: /cgn2_6/ptodata/1/pna/US0935_COMB.seq.*
- 109: /cgn2_6/ptodata/1/pna/US0934_COMB.seq.*
- 110: /cgn2_6/ptodata/1/pna/US0933_COMB.seq.*
- 111: /cgn2_6/ptodata/1/pna/US0932_COMB.seq.*
- 112: /cgn2_6/ptodata/1/pna/US0931_COMB.seq.*
- 113: /cgn2_6/ptodata/1/pna/US0930_COMB.seq.*
- 114: /cgn2_6/ptodata/1/pna/US0929_COMB.seq.*
- 115: /cgn2_6/ptodata/1/pna/US0928_COMB.seq.*
- 116: /cgn2_6/ptodata/1/pna/US0927_COMB.seq.*

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:33:43 ; Search time 362.333 Seconds
(without alignments)
664.322 Million cell updates/sec

Title: US-09-581-528E-19

Sequence: 1 tctggctcggagatgagatgacacactggaagcc 36

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7400732 seqs, 3343137571 residues

Total number of hits satisfying chosen parameters: 14801464

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications NA.*
2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10I_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	34	94.4	221	US-10-957-311-8
2	34	94.4	221	US-10-957-311-9
3	26	72.2	121	US-09-818-875-4196
4	26	72.2	121	US-09-818-875-4197
5	26	72.2	121	US-09-818-875-4200
6	26	72.2	121	US-09-818-875-4201
7	26	72.2	121	US-09-818-875-4204

C	8	26	72.2	121	10	US-09-818-875-4205	Sequence 4205, Ap
C	9	26	72.2	121	10	US-09-818-875-4208	Sequence 4208, Ap
C	10	26	72.2	121	10	US-09-818-875-4209	Sequence 4209, Ap
C	11	26	72.2	121	17	US-10-209-787-4196	Sequence 4196, Ap
C	12	26	72.2	121	17	US-10-209-787-4197	Sequence 4197, Ap
C	13	26	72.2	121	17	US-10-209-787-4200	Sequence 4200, Ap
C	14	26	72.2	121	17	US-10-209-787-4201	Sequence 4201, Ap
C	15	26	72.2	121	17	US-10-209-787-4204	Sequence 4204, Ap
C	16	26	72.2	121	17	US-10-209-787-4205	Sequence 4205, Ap
C	17	26	72.2	121	17	US-10-209-787-4208	Sequence 4208, Ap
C	18	26	72.2	121	17	US-10-209-787-4209	Sequence 4209, Ap
C	19	26	72.2	121	17	US-10-261-185-4196	Sequence 4196, Ap
C	20	26	72.2	121	17	US-10-261-185-4197	Sequence 4197, Ap
C	21	26	72.2	121	17	US-10-261-185-4200	Sequence 4200, Ap
C	22	26	72.2	121	17	US-10-261-185-4201	Sequence 4201, Ap
C	23	26	72.2	121	17	US-10-261-185-4204	Sequence 4204, Ap
C	24	26	72.2	121	17	US-10-261-185-4205	Sequence 4205, Ap
C	25	26	72.2	121	17	US-10-261-185-4208	Sequence 4208, Ap
C	26	26	72.2	121	17	US-10-261-185-4209	Sequence 4209, Ap
C	27	26	72.2	121	19	US-10-681-074-4196	Sequence 4196, Ap
C	28	26	72.2	121	19	US-10-681-074-4197	Sequence 4197, Ap
C	29	26	72.2	121	19	US-10-681-074-4200	Sequence 4200, Ap
C	30	26	72.2	121	19	US-10-681-074-4201	Sequence 4201, Ap
C	31	26	72.2	121	19	US-10-681-074-4204	Sequence 4204, Ap
C	32	26	72.2	121	19	US-10-681-074-4205	Sequence 4205, Ap
C	33	26	72.2	121	19	US-10-681-074-4208	Sequence 4208, Ap
C	34	26	72.2	121	19	US-10-681-074-4209	Sequence 4209, Ap
C	35	26	72.2	121	16	US-10-029-386-18073	Sequence 18073, A
C	36	26	72.2	121	16	US-10-029-386-4373	Sequence 4373, A
C	37	26	72.2	1254	22	US-10-504-173-4	Sequence 4, Appl
C	38	26	72.2	1392	9	US-09-895-035-13	Sequence 13, Appl
C	39	26	72.2	1392	20	US-10-888-004-13	Sequence 13, Appl
C	40	26	72.2	1404	9	US-09-754-949-3	Sequence 3, Appl
C	41	26	72.2	1404	10	US-09-896-621B-1	Sequence 1, Appl
C	42	26	72.2	1404	10	US-09-896-621B-2	Sequence 2, Appl
C	43	26	72.2	1404	10	US-09-896-621B-3	Sequence 3, Appl
C	44	26	72.2	1404	17	US-10-417-422-3	Sequence 3, Appl
C	45	26	72.2	2763	16	US-10-293-000-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-957-311-8
; Sequence 8, Application US/10957311
; Publication No. US20050076400A1
; GENERAL INFORMATION:
; APPLICANT: CASAS LOUZAQ, Cely
; APPLICANT: BENOIT, Patrick
; APPLICANT: PRADIER, Laurent
; APPLICANT: TREMP, Gunter
; APPLICANT: ITIER, Jean-Michel
; APPLICANT: BLANCHARD, Veronique
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXHIBITING MAJOR DISORDERS RELATED TO
; FILE REFERENCE: FRAV2003/0027 US NP
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US/10/957,311
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: FR 0311578
; PRIOR FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 221
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Murine Psi Exon 7 Containing Mutations
US-10-957-311-8

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:32:48 ; Search time 1275.67 Seconds
(without alignments)
386.247 Million cell updates/sec

Title: US-09-581-528E-18

Sequence: 1 tctgtcggagatgacatgcccacccatggaagccc 36

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 25053377 seqs, 6843368929 residues

Total number of hits satisfying chosen parameters: 50106754

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Pending Patents NA New:*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:2:1
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:2:1
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:4
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:4
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:4
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:4
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:1
8: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:2
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:10
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:10
11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:11
12: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:11
13: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:11
14: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:11
15: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:11
16: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:11
17: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:11
18: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:11
19: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:11
20: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:11
21: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:11
22: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:11
23: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:11
24: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:11
25: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:11
26: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:11

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34.8	96.7	36	US-09-581-528E-7	Sequence 7, Appl1
2	34.8	96.7	36	US-09-581-528E-8	Sequence 8, Appl1
3	34.8	96.7	36	US-09-581-528E-18	Sequence 18, Appl1
4	34.8	96.7	36	US-09-581-528E-19	Sequence 19, Appl1
5	34	94.4	1404	US-09-581-528E-4	Sequence 4, Appl1
6	34	94.4	1929	US-11-070-405-3	Sequence 3, Appl1
7	34	94.4	1964	US-11-070-405-135	Sequence 135, App

8	33.2	92.2	36	US-09-581-528E-20	Sequence 20, Appl1
9	32.4	90.0	1407	PCT-US04-42360-2316	Sequence 2316, Ap
10	32.4	90.0	1407	US-11-136-527-2454	Sequence 2454, Ap
11	26.8	74.4	201	US-60-659-397-5930	Sequence 5930, Ap
12	26.8	74.4	201	US-60-659-397-5931	Sequence 5931, Ap
13	26.8	74.4	201	US-60-659-397-5932	Sequence 5932, Ap
14	26.8	74.4	201	US-60-659-397-5933	Sequence 5933, Ap
15	26.8	74.4	201	US-60-659-397-5934	Sequence 5934, Ap
16	26.8	74.4	201	US-60-659-397-5935	Sequence 5935, Ap
17	26.8	74.4	201	US-60-659-397-5936	Sequence 5936, Ap
18	26.8	74.4	201	US-60-659-397-5937	Sequence 5937, Ap
19	26.8	74.4	201	US-60-659-397-5938	Sequence 5938, Ap
20	26.8	74.4	201	US-60-659-397-5939	Sequence 5939, Ap
21	26.8	74.4	201	US-60-659-397-5940	Sequence 5940, Ap
22	26.8	74.4	201	US-60-659-397-5941	Sequence 5941, Ap
23	26.8	74.4	201	US-60-659-397-5942	Sequence 5942, Ap
24	26.8	74.4	201	US-60-659-397-5943	Sequence 5943, Ap
25	26.8	74.4	201	US-60-659-397-5944	Sequence 5944, Ap
26	26.8	74.4	201	US-60-659-397-5945	Sequence 5945, Ap
27	26.8	74.4	201	US-60-659-397-5946	Sequence 5946, Ap
28	26.8	74.4	201	US-60-659-397-5947	Sequence 5947, Ap
29	26.8	74.4	201	US-60-659-397-5948	Sequence 5948, Ap
30	26.8	74.4	201	US-60-659-397-5949	Sequence 5949, Ap
31	26.8	74.4	201	US-60-659-397-5950	Sequence 5950, Ap
32	26.8	74.4	201	US-60-659-397-5951	Sequence 5951, Ap
33	26.8	74.4	201	US-60-659-397-5952	Sequence 5952, Ap
34	26.8	74.4	201	US-60-659-397-5953	Sequence 5953, Ap
35	26.8	74.4	201	US-60-659-397-5954	Sequence 5954, Ap
36	26.8	74.4	201	US-60-659-397-5955	Sequence 5955, Ap
37	26.8	74.4	201	US-60-659-397-5956	Sequence 5956, Ap
38	26.8	74.4	201	US-60-659-397-5957	Sequence 5957, Ap
39	26.8	74.4	201	US-60-659-397-5958	Sequence 5958, Ap
40	26.8	74.4	201	US-60-659-397-5959	Sequence 5959, Ap
41	26.8	74.4	201	US-60-659-397-5960	Sequence 5960, Ap
42	26.8	74.4	201	US-60-659-397-5961	Sequence 5961, Ap
43	26.8	74.4	201	US-60-659-397-5962	Sequence 5962, Ap
44	26.8	74.4	201	US-60-659-397-5963	Sequence 5963, Ap
45	26.8	74.4	201	US-60-659-397-5964	Sequence 5964, Ap

ALIGNMENTS

RESULT 1
US-09-581-528E-7
Sequence 7, Application US/09581528E
GENERAL INFORMATION:
APPLICANT: TAKEDA, Masatoshi
TITLE OF INVENTION: Gene Mutant Animals
FILE REFERENCE: P19743
CURRENT APPLICATION NUMBER: US/09/581,528E
PRIOR FILING DATE: 1999-01-07
PCT/J99/00015
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Primer
US-09-581-528E-7

Query Match 96.7%; Score 34.8; DB 6; Length 36;
Best Local Similarity 94.4%; Pred. No. 0.00037;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTGTCGGAGATGATGCAVCCACTGGAAGGCC 36
DB 1 TGTGTCGGAGATGATGCAVCCACTGGAAGGCC 36

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:29:14 ; Search time 2455 Seconds
(without alignments)
598.627 Million cell updates/sec

Title: US-09-581-528E-18

Perfect score: 36
Sequence: 1 tctggtcgagatgacgacccactggaagagccc 36

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_Main:*

- 1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/PCTUS3_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
- 14: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
- 15: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
- 16: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
- 17: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
- 18: /cgn2_6/ptodata/1/pna/US092A_COMB.seq:*
- 19: /cgn2_6/ptodata/1/pna/US092B_COMB.seq:*
- 20: /cgn2_6/ptodata/1/pna/US093A_COMB.seq:*
- 21: /cgn2_6/ptodata/1/pna/US093B_COMB.seq:*
- 22: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
- 23: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
- 24: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
- 25: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
- 26: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
- 27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
- 28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
- 29: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
- 30: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
- 31: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
- 32: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
- 33: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
- 34: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
- 35: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
- 36: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
- 37: /cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
- 38: /cgn2_6/ptodata/1/pna/US098D_COMB.seq:*
- 39: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
- 40: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
- 41: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
- 42: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
- 43: /cgn2_6/ptodata/1/pna/US099E_COMB.seq:*

- 44: /cgn2_6/ptodata/1/pna/US099F_COMB.seq:*
- 45: /cgn2_6/ptodata/1/pna/US099G_COMB.seq:*
- 46: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
- 47: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:*
- 48: /cgn2_6/ptodata/1/pna/US101A_COMB.seq:*
- 49: /cgn2_6/ptodata/1/pna/US101B_COMB.seq:*
- 50: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*
- 51: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*
- 52: /cgn2_6/ptodata/1/pna/US103A_COMB.seq:*
- 53: /cgn2_6/ptodata/1/pna/US103B_COMB.seq:*
- 54: /cgn2_6/ptodata/1/pna/US104A_COMB.seq:*
- 55: /cgn2_6/ptodata/1/pna/US104B_COMB.seq:*
- 56: /cgn2_6/ptodata/1/pna/US105A_COMB.seq:*
- 57: /cgn2_6/ptodata/1/pna/US105B_COMB.seq:*
- 58: /cgn2_6/ptodata/1/pna/US106A_COMB.seq:*
- 59: /cgn2_6/ptodata/1/pna/US107A_COMB.seq:*
- 60: /cgn2_6/ptodata/1/pna/US107B_COMB.seq:*
- 61: /cgn2_6/ptodata/1/pna/US107C_COMB.seq:*
- 62: /cgn2_6/ptodata/1/pna/US108A_COMB.seq:*
- 63: /cgn2_6/ptodata/1/pna/US108B_COMB.seq:*
- 64: /cgn2_6/ptodata/1/pna/US109A_COMB.seq:*
- 65: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:*
- 66: /cgn2_6/ptodata/1/pna/US109C_COMB.seq:*
- 67: /cgn2_6/ptodata/1/pna/US109D_COMB.seq:*
- 68: /cgn2_6/ptodata/1/pna/US110_COMB.seq:*
- 69: /cgn2_6/ptodata/1/pna/US6000_COMB.seq:*
- 70: /cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
- 71: /cgn2_6/ptodata/1/pna/US6002_COMB.seq:*
- 72: /cgn2_6/ptodata/1/pna/US6003_COMB.seq:*
- 73: /cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
- 74: /cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
- 75: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
- 76: /cgn2_6/ptodata/1/pna/US6007_COMB.seq:*
- 77: /cgn2_6/ptodata/1/pna/US6008_COMB.seq:*
- 78: /cgn2_6/ptodata/1/pna/US6009_COMB.seq:*
- 79: /cgn2_6/ptodata/1/pna/US6010_COMB.seq:*
- 80: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
- 81: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
- 82: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:*
- 83: /cgn2_6/ptodata/1/pna/US6014_COMB.seq:*
- 84: /cgn2_6/ptodata/1/pna/US6015_COMB.seq:*
- 85: /cgn2_6/ptodata/1/pna/US6016_COMB.seq:*
- 86: /cgn2_6/ptodata/1/pna/US6017_COMB.seq:*
- 87: /cgn2_6/ptodata/1/pna/US6018_COMB.seq:*
- 88: /cgn2_6/ptodata/1/pna/US6019_COMB.seq:*
- 89: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:*
- 90: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:*
- 91: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
- 92: /cgn2_6/ptodata/1/pna/US6023A_COMB.seq:*
- 93: /cgn2_6/ptodata/1/pna/US6023B_COMB.seq:*
- 94: /cgn2_6/ptodata/1/pna/US6024_COMB.seq:*
- 95: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
- 96: /cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
- 97: /cgn2_6/ptodata/1/pna/US6027_COMB.seq:*
- 98: /cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
- 99: /cgn2_6/ptodata/1/pna/US6029_COMB.seq:*
- 100: /cgn2_6/ptodata/1/pna/US6030_COMB.seq:*
- 101: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
- 102: /cgn2_6/ptodata/1/pna/US6032_COMB.seq:*
- 103: /cgn2_6/ptodata/1/pna/US6033_COMB.seq:*
- 104: /cgn2_6/ptodata/1/pna/US6034_COMB.seq:*
- 105: /cgn2_6/ptodata/1/pna/US6035_COMB.seq:*
- 106: /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
- 107: /cgn2_6/ptodata/1/pna/US6037_COMB.seq:*
- 108: /cgn2_6/ptodata/1/pna/US6038_COMB.seq:*
- 109: /cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
- 110: /cgn2_6/ptodata/1/pna/US6040_COMB.seq:*
- 111: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*
- 112: /cgn2_6/ptodata/1/pna/US6042_COMB.seq:*
- 113: /cgn2_6/ptodata/1/pna/US6043_COMB.seq:*
- 114: /cgn2_6/ptodata/1/pna/US6044_COMB.seq:*
- 115: /cgn2_6/ptodata/1/pna/US6045_COMB.seq:*
- 116: /cgn2_6/ptodata/1/pna/US6046_COMB.seq:*

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2005, 18:15:32 ; Search time 90 Seconds
(without alignments)
2112.009 Million cell updates/sec

Title: US-09-581-528E-3

Perfect score: 2399
Sequence: 1 MFEIRAPAPLSTFQNAQMSBDS.....ATDIYVQPFMDQLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 1826554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodacata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodacata/1/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodacata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodacata/1/pubppaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodacata/1/pubppaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodacata/1/pubppaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodacata/1/pubppaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodacata/1/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodacata/1/pubppaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodacata/1/pubppaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodacata/1/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodacata/1/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodacata/1/pubppaa/US10B_PUBCOMB.pep:*
- 14: /cgn2_6/ptodacata/1/pubppaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/ptodacata/1/pubppaa/US10D_PUBCOMB.pep:*
- 16: /cgn2_6/ptodacata/1/pubppaa/US10E_PUBCOMB.pep:*
- 17: /cgn2_6/ptodacata/1/pubppaa/US10F_PUBCOMB.pep:*
- 18: /cgn2_6/ptodacata/1/pubppaa/US10G_PUBCOMB.pep:*
- 19: /cgn2_6/ptodacata/1/pubppaa/US10H_PUBCOMB.pep:*
- 20: /cgn2_6/ptodacata/1/pubppaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodacata/1/pubppaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodacata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2374	99.2	467	17	US-10-957-311-3
2	2240	93.6	467	16	US-10-811-199-2
3	2239	93.6	467	9	US-09-754-949-4
4	2239	93.6	467	9	US-09-895-035-14
5	2239	93.6	467	9	US-09-895-035-14
6	2239	93.6	467	13	US-10-071-900-1
7	2239	93.6	467	14	US-10-221-254-4
8	2239	93.6	467	14	US-10-180-781-3
9	2239	93.6	467	15	US-10-417-422-4
10	2239	93.6	467	15	US-10-888-004-14
11	2239	93.6	467	17	US-10-221-291-3

12	2234	93.4	467	9	US-09-785-474-2	Sequence 2, Appli
13	2229	93.1	467	9	US-09-785-474-32	Sequence 32, Appli
14	2229	93.1	467	10	US-09-896-621B-4	Sequence 4, Appli
15	2227	93.1	467	10	US-09-896-621B-5	Sequence 5, Appli
16	2224	92.9	467	9	US-09-785-474-30	Sequence 30, Appli
17	2222	92.9	467	9	US-09-785-474-28	Sequence 28, Appli
18	2217	92.6	467	10	US-09-896-621B-6	Sequence 6, Appli
19	2210	92.4	463	9	US-09-895-035-12	Sequence 12, Appli
20	2210	92.4	463	16	US-10-888-004-12	Sequence 12, Appli
21	2207	92.2	467	9	US-09-785-474-4	Sequence 4, Appli
22	2198	91.4	467	14	US-10-293-000-5	Sequence 5, Appli
23	1468	61.3	448	9	US-09-878-454A-1	Sequence 1, Appli
24	1468	61.3	448	13	US-10-071-900-2	Sequence 2, Appli
25	1468	61.3	448	14	US-10-293-000-6	Sequence 6, Appli
26	1468	61.3	448	14	US-10-180-781-2	Sequence 2, Appli
27	1463	61.1	448	16	US-10-811-199-9	Sequence 9, Appli
28	1460	61.0	448	9	US-09-754-949-6	Sequence 6, Appli
29	1460	61.0	448	14	US-10-221-254-6	Sequence 6, Appli
30	1460	61.0	448	15	US-10-417-422-6	Sequence 5, Appli
31	1460	61.0	448	17	US-10-221-291-5	Sequence 10, Appli
32	1450	60.6	448	10	US-09-896-621B-10	Sequence 11, Appli
33	1448	60.5	448	10	US-09-896-621B-11	Sequence 12, Appli
34	1438	60.1	448	10	US-09-896-621B-12	Sequence 1, Appli
35	985.5	41.2	461	16	US-10-811-199-1	Sequence 6, Appli
36	985.5	41.2	461	16	US-10-811-199-6	Sequence 1, Appli
37	717.5	30.0	180	9	US-09-895-035-1	Sequence 1, Appli
38	717.5	30.0	180	16	US-10-888-004-1	Sequence 8, Appli
39	591.5	24.7	354	9	US-09-823-153-8	Sequence 8, Appli
40	591.5	24.7	354	16	US-10-713-981-8	Sequence 60796, A
41	562.5	23.5	478	15	US-10-425-114-60796	Sequence 352586, A
42	562.5	23.5	478	16	US-10-425-114-352586	Sequence 47501, A
43	562.5	23.5	491	15	US-10-425-114-47501	Sequence 166498, A
44	543.5	22.7	436	16	US-10-437-963-166498	Sequence 3, Appli
45	507	21.2	157	16	US-10-811-199-3	

ALIGNMENTS

RESULT 1
US-10-957-311-3
Sequence 3, Application US/10957311
Publication No. US20050076400A1
GENERAL INFORMATION:
APPLICANT: CASAS LOUZA, Cely
APPLICANT: BENOIT, Patrick
APPLICANT: PRADIER, Laurent
APPLICANT: TREMP, Gunter
APPLICANT: ITRER, Jean-Michel
APPLICANT: BLANCHARD, Veronique
TITLE OF INVENTION: TRANSGENIC ANIMALS EXHIBITING MAJOR DISORDERS RELATED TO
FILE REFERENCE: FRAV2003/0027 US NP
CURRENT APPLICATION NUMBER: US/10/957,311
CURRENT FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: US 60/523,397
PRIOR FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: FR 0311578
PRIOR FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 467
TYPE: PRT
ORGANISM: Artificialat
FEATURE:
OTHER INFORMATION: Murine P51 Protein with Mutations M233T and I235P
US-10-957-311-3
Query Match 99.2% Score 2374; DB 17; Length 467;
Best Local Similarity 99.1% Pred. No. 1.3e-203;
Matches 463; Conservative 2; Mismatches 2; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2005, 16:28:22 / Search time 31 Seconds
(without alignments)
1124.552 Million cell updates/sec

Title: US-09-581-528E-3

Perfect score: 2393
Sequence: 1 MTEIPAPLSTYFONQMSBDS.....ATDYIVQFMDQLAHQFYI 467

Scoring table: GAPOP 10.0, Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUTS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/bacfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	2387	99.7	467 3	US-08-888-077A-17 Sequence 17, Appl
2	2387	99.7	467 3	US-08-496-841C-136 Sequence 136, App
3	2366	98.9	465 4	US-09-496-239A-18 Sequence 18, Appl
4	2337	97.7	467 2	US-08-967-101-4 Sequence 4, Appl
5	2337	97.7	467 2	US-08-592-541-4 Sequence 4, Appl
6	2337	97.7	467 3	US-09-124-698-4 Sequence 4, Appl
7	2337	97.7	467 3	US-09-127-480-4 Sequence 4, Appl
8	2337	97.7	467 3	US-08-496-841C-4 Sequence 4, Appl
9	2337	97.7	467 3	US-09-124-523-4 Sequence 4, Appl
10	2337	97.7	467 4	US-09-636-796A-4 Sequence 4, Appl
11	2337	97.7	467 4	US-08-431-048F-4 Sequence 4, Appl
12	2335	97.5	465 3	US-08-788-231A-17 Sequence 17, Appl
13	2240	93.6	467 4	US-09-043-944-2 Sequence 2, Appl
14	2239	93.6	467 2	US-08-967-101-134 Sequence 134, App
15	2239	93.6	467 2	US-08-592-541-134 Sequence 134, App
16	2239	93.6	467 3	US-08-923-454A-10 Sequence 10, Appl
17	2239	93.6	467 3	US-08-670-964-2 Sequence 2, Appl
18	2239	93.6	467 3	US-08-888-077A-2 Sequence 2, Appl
19	2239	93.6	467 3	US-09-124-698-134 Sequence 134, App
20	2239	93.6	467 3	US-09-127-480-134 Sequence 134, App
21	2239	93.6	467 3	US-08-496-841C-134 Sequence 134, App
22	2239	93.6	467 3	US-08-832-867-3 Sequence 3, Appl
23	2239	93.6	467 3	US-09-227-725A-1 Sequence 1, Appl
24	2239	93.6	467 3	US-09-124-523-134 Sequence 134, App
25	2239	93.6	467 4	US-09-375-318-3 Sequence 3, Appl
26	2239	93.6	467 4	US-09-636-796A-134 Sequence 134, App
27	2239	93.6	467 4	US-09-895-035-14 Sequence 14, Appl

28	2239	93.6	467 4	US-09-501-171-1 Sequence 1, Appl
29	2239	93.6	467 4	US-09-949-016-5873 Sequence 5873, Ap
30	2239	93.6	487 4	US-09-949-016-9173 Sequence 9173, Ap
31	2239	93.6	487 4	US-09-949-016-9174 Sequence 9174, Ap
32	2239	93.6	487 4	US-09-949-016-9175 Sequence 9175, Ap
33	2234	93.4	467 3	US-08-706-344C-2 Sequence 2, Appl
34	2233	93.3	467 2	US-08-967-101-2 Sequence 2, Appl
35	2233	93.3	467 2	US-08-592-541-2 Sequence 2, Appl
36	2233	93.3	467 3	US-09-124-698-2 Sequence 2, Appl
37	2233	93.3	467 3	US-09-127-480-2 Sequence 2, Appl
38	2233	93.3	467 3	US-08-496-841C-2 Sequence 2, Appl
39	2233	93.3	467 3	US-09-124-523-2 Sequence 2, Appl
40	2233	93.3	467 4	US-09-636-796A-2 Sequence 2, Appl
41	2233	93.3	467 4	US-08-431-048F-2 Sequence 2, Appl
42	2229	93.1	467 3	US-08-706-344C-32 Sequence 32, Appl
43	2229	93.1	467 4	US-09-896-621B-4 Sequence 4, Appl
44	2227	93.1	467 4	US-09-896-621B-5 Sequence 5, Appl
45	2224	92.9	467 3	US-08-706-344C-30 Sequence 30, Appl

ALIGNMENTS

```
RESULT 1
US-08-888-077A-17
; Sequence 17, Application US/08888077A
; Patent No. 6020143
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LERNER, DAVID, LITTENBERG, KRUMHOLTZ & MENTLIK
; STREET: 600 SOUTH AVENUE WEST
; CITY: WESTFIELD
; STATE: NJ
; COUNTRY: USA
; ZIP: 07090-1497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,077A
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,541
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: PALISI, THOMAS M
; REGISTRATION NUMBER: 36,629
; REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 654-5000
; TELEFAX: (908) 654-7866
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-077A-17
```

Query Match 99.7%, Score 2387, DB 3, Length 467;
Best Local Similarity 99.6%, Pred. No. 2.8e-235;
Matches 465; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEIPAPLSTYFONQMSBDSHSSAIIKNSQNDSEKQQQHQRLDNEPPIINGRQNSNR 60